

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Atty. Docket No: 077319/0125

In re patent application of

David W. LEUNG et al.

Serial No. 08/842,827

Group Art Unit: 1801

Filed: April 17, 1997

Examiner: Unassigned

For: HUMAN PHOSPHATIDIC ACID PHOSPHATASE

STATEMENT TO SUPPORT FILING AND SUBMISSION IN ACCORDANCE
WITH 37 C.F.R. §§ 1.821-1.825

Assistant Commissioner for Patents
Washington, D.C. 20231
Box SEQUENCE

Sir:

In connection with a Sequence Listing submitted concurrently herewith, the undersigned hereby states that:

1. the submission, filed herewith in accordance with 37 C.F.R. § 1.821(g), does not include new matter; and

2. the content of the attached paper copy and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same.

Respectfully submitted,

5 August 1997
Date

Stephen A. Bent
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Reg. No. 29,768

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: LEUNG, David W.
TOMPKINS, Christopher K.
- (ii) TITLE OF INVENTION: HUMAN PHOSPHATIDIC ACID PHOSPHATASE
- (iii) NUMBER OF SEQUENCES: 21
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Foley & Lardner
 - (B) STREET: 3000 K Street, N.W., Suite 500
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: USA
 - (F) ZIP: 20007-5109
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/842,827
 - (B) FILING DATE: 17-APR-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: BENT, Stephen A.
 - (B) REGISTRATION NUMBER: 29,768
 - (C) REFERENCE/DOCKET NUMBER: 77319/125
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (202)672-5300
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 - (C) TELEX: 904136

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1563 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 342..1193

- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 342..1193

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCTGTGGGAG AGAGCGCCGG GATCCGGACG GGGTAGCAAC CGGGGCAGGC CGTGCCGGCT	60
GAGGAGGTCC TGAGGCTACA GAGCTGCCGC GGCTGGCACA CGAGCGCCTC GGCACCTAACC	120

GAGTGTTCGC	GGGGGCTGTG	AGGGGAGGGC	CCCGGGCGCC	ATTGCTGGCG	GTGGGAGCGC	180
CGCCCCGGTCT	CAGCCCCGCC	TCGGCTGCTC	TCCTCCTCCG	GCTGGGAGGG	GCCGTATCTC	240
GGGGCCGTCG	CCAGCCCCGG	CCCGGGCTCG	ATAATCAAGG	GCCTCGGCCG	TCGTCCCGCA	300
CCTCATTTCCA	TCGCCCTTGC	CGGGCAGCCC	GGGCAGAGAC	C ATG TTT GAC AAG		353
				Met Phe Asp Lys		
				1		
ACG CGG CTG CCG TAC GTG GCC CTC GAT GTG CTC TGC GTG TTG CTG GCT	Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys Val Leu Leu Ala	5 10 15 20				401
GGA TTG CCT TTT GCA ATT CTT ACT TCA AGG CAT ACC CCC TTC CAA CGA	Gly Leu Pro Phe Ala Ile Leu Thr Ser Arg His Thr Pro Phe Gln Arg	25 30 35				449
GGA GTA TTC TGT AAT GAT GAG TCC ATC AAG TAC CCT TAC AAA GAA GAC	Gly Val Phe Cys Asn Asp Glu Ser Ile Lys Tyr Pro Tyr Lys Glu Asp	40 45 50				497
ACC ATA CCT TAT GCG TTA TTA GGT GGA ATA ATC ATT CCA TTC AGT ATT	Thr Ile Pro Tyr Ala Leu Leu Gly Gly Ile Ile Ile Pro Phe Ser Ile	55 60 65				545
ATC GTT ATT ATT CTT GGA GAA ACC CTG TCT GTT TAC TGT AAC CTT TTG	Ile Val Ile Ile Leu Gly Glu Thr Leu Ser Val Tyr Cys Asn Leu Leu	70 75 80				593
CAC TCA AAT TCC TTT ATC AGG AAT AAC TAC ATA GCC ACT ATT TAC AAA	His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile Ala Thr Ile Tyr Lys	85 90 95 100				641
GCC ATT GGA ACC TTT TTA TTT GGT GCA GCT GCT AGT CAG TCC CTG ACT	Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ala Ser Gln Ser Leu Thr	105 110 115				689
GAC ATT GCC AAG TAT TCA ATA GGC AGA CTG CGG CCT CAC TTC TTG GAT	Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg Pro His Phe Leu Asp	120 125 130				737
GTT TGT GAT CCA GAT TGG TCA AAA ATC AAC TGC AGC GAT GGT TAC ATT	Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys Ser Asp Gly Tyr Ile	135 140 145				785
GAA TAC TAC ATA TGT CGA GGG AAT GCA GAA AGA GTT AAG GAA GGC AGG	Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg Val Lys Glu Gly Arg	150 155 160				833
TTG TCC TTC TAT TCA GGC CAC TCT TCG TTT TCC ATG TAC TGC ATG CTG	Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met Tyr Cys Met Leu	165 170 175 180				881
TTT GTG GCA CTT TAT CTT CAA GCC AGG ATG AAG GGA GAC TGG GCA AGA	Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly Asp Trp Ala Arg	185 190 195				929
CTC TTA CGC CCC ACA CTG CAA TTT GGT CTT GTT GCC GTA TCC ATT TAT	Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val Ala Val Ser Ile Tyr	200 205 210				977
GTG GGC CTT TCT CGA GTT TCT GAT TAT AAA CAC CAC TGG AGC GAT GTG	Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His Trp Ser Asp Val	215 220 225				1025

TTG ACT GGA CTC ATT CAG GGA GCT CTG GTT GCA ATA TTA GTT GCT GTA	1073
Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala Ile Leu Val Ala Val	
230 235 240	
TAT GTA TCG GAT TTC TTC AAA GAA AGA ACT TCT TTT AAA GAA AGA AAA	1121
Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe Lys Glu Arg Lys	
245 250 255 260	
GAG GAG GAC TCT CAT ACA ACT CTG CAT GAA ACA CCA ACA ACT GGG AAT	1169
Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro Thr Thr Gly Asn	
265 270 275	
CAC TAT CCG AGC AAT CAC CAG CCT TGAAAGGCAG CAGGGTGCCC AGGTGAAGCT	1223
His Tyr Pro Ser Asn His Gln Pro	
280	
GGCCTGTTTT CTAAAGGAAA ATGATTGCCA CAAGGCAAGA GGATGCATCT TTCTTCCTGG	1283
TGTACAAGCC TTAAAGACT TCTGCTGCTG ATATGCCTCT TGGATGCACA CTTTGTGTGT	1343
ACATAGTTAC CTTTAACTCA GTGGTTATCT AATAGCTCTA AACTCATTA AAAAACTCCA	1403
AGCCTTCCAC CAAAACAGTG CCCACCTGT ATACATTTTT ATTA AAAAAA TGTAATGCTT	1463
ATGTATAAAC ATGTATGTAA TATGCTTTCT ATGAATGATG TTTGATTAA ATATAATACA	1523
TATTAAATG TATGGGAGAA CCA AAAAAA AAAAAA	1563

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 284 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Phe	Asp	Lys	Thr	Arg	Leu	Pro	Tyr	Val	Ala	Leu	Asp	Val	Leu	Cys
1				5					10					15	
Val	Leu	Leu	Ala	Gly	Leu	Pro	Phe	Ala	Ile	Leu	Thr	Ser	Arg	His	Thr
			20					25					30		
Pro	Phe	Gln	Arg	Gly	Val	Phe	Cys	Asn	Asp	Glu	Ser	Ile	Lys	Tyr	Pro
		35					40					45			
Tyr	Lys	Glu	Asp	Thr	Ile	Pro	Tyr	Ala	Leu	Leu	Gly	Gly	Ile	Ile	Ile
	50					55					60				
Pro	Phe	Ser	Ile	Ile	Val	Ile	Ile	Leu	Gly	Glu	Thr	Leu	Ser	Val	Tyr
	65				70					75					80
Cys	Asn	Leu	Leu	His	Ser	Asn	Ser	Phe	Ile	Arg	Asn	Asn	Tyr	Ile	Ala
				85					90					95	
Thr	Ile	Tyr	Lys	Ala	Ile	Gly	Thr	Phe	Leu	Phe	Gly	Ala	Ala	Ala	Ser
			100					105					110		
Gln	Ser	Leu	Thr	Asp	Ile	Ala	Lys	Tyr	Ser	Ile	Gly	Arg	Leu	Arg	Pro
		115					120					125			
His	Phe	Leu	Asp	Val	Cys	Asp	Pro	Asp	Trp	Ser	Lys	Ile	Asn	Cys	Ser
	130					135					140				

Asp Gly Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg Val
145 150 155 160

Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met
165 170 175

Tyr Cys Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly
180 185 190

Asp Trp Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val Ala
195 200 205

Val Ser Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His
210 215 220

Trp Ser Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala Ile
225 230 235 240

Leu Val Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe
245 250 255

Lys Glu Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro
260 265 270

Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro
275 280

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1566 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 342..1196

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 342..1196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCTGTGGGAG AGAGCGCCGG GATCCGGACG GGGTAGCAAC CGGGGCAGGC CGTGCCGGCT	60
GAGGAGGTCC TGAGGCTACA GAGCTGCCGC GGCTGGCACA CGAGCGCCTC GGCACATAACC	120
GAGTGTTTCGC GGGGGCTGTG AGGGGAGGGC CCCGGGCGCC ATTGCTGGCG GTGGGAGCGC	180
CGCCCGGTCT CAGCCCCGCC TCGGCTGCTC TCCTCCTCCG GCTGGGAGGG GCCGTATCTC	240
GGGGCCGTCG CCAGCCCCGG CCCGGGCTCG ATAATCAAGG GCCTCGGCCG TCGTCCCGCA	300
CCTCATTTCA TCGCCCTTGC CGGGCAGCCC GGGCAGAGAC C ATG TTT GAC AAG	353
Met Phe Asp Lys	
1	
ACG CGG CTG CCG TAC GTG GCC CTC GAT GTG CTC TGC GTG TTG CTG GCT	401
Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys Val Leu Leu Ala	
5 10 15 20	

AGGTGAAGCT	GGCCTGTTTT	CTAAAGGAAA	ATGATTGCCA	CAAGGCAAGA	GGATGCATCT	1276
TTCTTCCTGG	TGTACAAGCC	TTTAAAGACT	TCTGCTGCTG	ATATGCCTCT	TGGATGCACA	1336
CTTTGTGTGT	ACATAGTTAC	CTTTAACTCA	GTGGTTATCT	AATAGCTCTA	AACTCATTA	1396
AAAAACTCCA	AGCCTTCCAC	CAAAACAGTG	CCCCACCTGT	ATACATTTTT	ATTAAAAAAA	1456
TGTAATGCTT	ATGTATAAAC	ATGTATGTAA	TATGCTTTCT	ATGAATGATG	TTTGATTTAA	1516
ATATAATACA	TATTAAATG	TATGGGAGAA	CCAAAAAAA	AAAAAAA		1566

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 285 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Phe	Asp	Lys	Thr	Arg	Leu	Pro	Tyr	Val	Ala	Leu	Asp	Val	Leu	Cys
1				5					10					15	
Val	Leu	Leu	Ala	Ser	Met	Pro	Met	Ala	Val	Leu	Lys	Leu	Gly	Gln	Ile
			20					25					30		
Tyr	Pro	Phe	Gln	Arg	Gly	Phe	Phe	Cys	Lys	Asp	Asn	Ser	Ile	Asn	Tyr
		35				40					45				
Pro	Tyr	His	Asp	Ser	Thr	Ala	Ala	Ser	Thr	Val	Leu	Ile	Leu	Val	Gly
	50					55					60				
Val	Gly	Leu	Pro	Val	Ser	Ser	Ile	Ile	Leu	Gly	Glu	Thr	Leu	Ser	Val
	65				70					75					80
Tyr	Cys	Asn	Leu	Leu	His	Ser	Asn	Ser	Phe	Ile	Ser	Asn	Asn	Tyr	Ile
			85						90					95	
Ala	Thr	Ile	Tyr	Lys	Ala	Ile	Gly	Thr	Phe	Leu	Phe	Gly	Ala	Ala	Ala
			100					105					110		
Ser	Gln	Ser	Leu	Thr	Asp	Ile	Ala	Lys	Tyr	Ser	Ile	Gly	Arg	Leu	Arg
		115					120					125			
Pro	His	Phe	Leu	Asp	Val	Cys	Asp	Pro	Asp	Trp	Ser	Lys	Ile	Asn	Cys
	130					135					140				
Ser	Asp	Gly	Tyr	Ile	Glu	Tyr	Tyr	Ile	Cys	Arg	Gly	Asn	Ala	Glu	Arg
	145				150				155					160	
Val	Lys	Glu	Gly	Arg	Leu	Ser	Phe	Tyr	Ser	Gly	His	Ser	Ser	Phe	Ser
			165						170					175	
Met	Tyr	Cys	Met	Leu	Phe	Val	Ala	Leu	Tyr	Leu	Gln	Ala	Arg	Met	Lys
			180					185					190		
Gly	Asp	Trp	Ala	Arg	Leu	Leu	Arg	Pro	Thr	Leu	Gln	Phe	Gly	Leu	Val
	195						200					205			
Ala	Val	Ser	Ile	Tyr	Val	Gly	Leu	Ser	Arg	Val	Ser	Asp	Tyr	Lys	His
	210					215					220				

123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100101102103104105106107108109110111112113114115116117118119120121122123124125126127128129130131132133134135136137138139140141142143144145146147148149150151152153154155156157158159160161162163164165166167168169170171172173174175176177178179180181182183184185186187188189190191192193194195196197198199200201202203204205206207208209210211212213214215216217218219220221222223224225226227228229230231232233234235236237238239240241242243244245246247248249250251252253254255256257258259260261262263264265266267268269270271272273274275276277278279280281282283284285286287288289290291292293294295296297298299300

His Trp Ser Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala
 225 230 235 240
 Ile Leu Val Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser
 245 250 255
 Phe Lys Glu Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr
 260 265 270
 Pro Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro
 275 280 285

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 294..1226

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 294..1226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGCGCAGCTC TGCAAAAGTT TCTGCTCGGG ATCTGGCTCT CTTCCTTCTTG GACTTTAGAA 60
 CGATTTAGGG TTGACAGAGG AAAGCAGAGG CGCGCAGGAG GAGCAGAAAA CACCACCTTC 120
 TGCAGTTGGA GGCAGGCAGC CCCGGCTGCA CTCTAGCCGC CGCGCCCGGA GCCGGGGCCG 180
 ACCCGCCACT ATCCGCAGCA GCCTCGGCCA GGAGGCGACC CGGGCGCCTG GGTGTGTGGC 240
 TGCTGTTGCG GGACGTCTTC GCGGGGCGGG AGGCTCGCGC CGCAGCCAGC GCC ATG 296
 Met
 1
 CAA AAC TAC AAG TAC GAC AAA GCG ATC GTC CCG GAG AGC AAG AAC GGC 344
 Gln Asn Tyr Lys Tyr Asp Lys Ala Ile Val Pro Glu Ser Lys Asn Gly
 5 10 15
 GGC AGC CCG GCG CTC AAC AAC AAC CCG AGG AGG AGC GGC AGC AAG CGG 392
 Gly Ser Pro Ala Leu Asn Asn Pro Arg Arg Ser Gly Ser Lys Arg
 20 25 30
 GTG CTG CTC ATC TGC CTC GAC CTC TTC TGC CTC TTC ATG GCG GGC CTC 440
 Val Leu Leu Ile Cys Leu Asp Leu Phe Cys Leu Phe Met Ala Gly Leu
 35 40 45
 CCC TTC CTC ATC ATC GAG ACA AGC ACC ATC AAG CCT TAC CAC CGA GGG 488
 Pro Phe Leu Ile Ile Glu Thr Ser Thr Ile Lys Pro Tyr His Arg Gly
 50 55 60 65
 TTT TAC TGC AAT GAT GAG AGC ATC AAG TAC CCA CTG AAA ACT GGT GAG 536
 Phe Tyr Cys Asn Asp Glu Ser Ile Lys Tyr Pro Leu Lys Thr Gly Glu
 70 75 80

ACA Thr	ATA Ile	AAT Asn	GAC Asp 85	GCT Ala	GTG Val	CTC Leu	TGT Cys	GCC Ala 90	GTG Val	GGG Gly	ATC Ile	GTC Val	ATT Ile 95	GCC Ala	ATC Ile	584	
CTC Leu	GCG Ala	ATC Ile 100	ATC Ile	ACG Thr	GGG Gly	GAA Glu	TTC Phe 105	TAC Tyr	CGG Arg	ATC Ile	TAT Tyr	TAC Tyr 110	CTG Leu	AAG Lys	AAG Lys	632	
TCG Ser	CGG Arg 115	TCG Ser	ACG Thr	ATT Ile	CAG Gln	AAC Asn 120	CCC Pro	TAC Tyr	GTG Val	GCA Ala 125	GCA Ala	CTC Leu	TAT Tyr	AAG Lys	CAA Gln	680	
GTG Val 130	GGC Gly	TGC Cys	TTC Phe	CTC Leu	TTT Phe 135	GGC Gly	TGT Cys	GCC Ala	ATC Ile	AGC Ser 140	CAG Gln	TCT Ser	TTC Phe	ACA Thr	GAC Asp 145	728	
ATT Ile	GCC Ala	AAA Lys	GTG Val 150	TCC Ser	ATA Ile	GGG Gly	CGC Arg	CTG Leu	CGT Arg 155	CCT Pro	CAC His	TTC Phe	TTG Leu	AGT Ser 160	GTC Val	776	
TGC Cys	AAC Asn	CCT Pro	GAT Asp 165	TTC Phe	AGC Ser	CAG Gln	ATC Ile	AAC Asn 170	TGC Cys	TCT Ser	GAA Glu	GGC Gly 175	TAC Tyr 175	ATT Ile	CAG Gln	824	
AAC Asn	TAC Tyr	AGA Arg 180	TGC Cys	AGA Arg	GGT Gly	GAT Asp 185	GAC Asp	AGC Ser	AAA Lys	GTC Val	CAG Gln	GAA Glu 190	GCC Ala	AGG Arg	AAG Lys	872	
TCC Ser	TTC Phe 195	TTC Phe	TCT Ser	GGC Gly	CAT His	GCC Ala 200	TCC Ser	TTC Phe	TCC Ser	ATG Met	TAC Tyr 205	ACT Thr	ATG Met	CTG Leu	TAT Tyr	920	
TTG Leu 210	GTG Val	CTA Leu	TAC Tyr	CTG Leu	CAG Gln 215	GCC Ala	CGC Arg	TTC Phe	ACT Thr	TGG Trp 220	CGA Arg	GGA Gly	GCC Ala	CGC Arg	CTG Leu 225	968	
CTC Leu	CGG Arg	CCC Pro	CTC Leu	CTG Leu 230	CAG Gln	TTC Phe	ACC Thr	TTG Leu	ATC Ile 235	ATG Met	ATG Met	GCC Ala	TTC Phe	TAC Tyr 240	ACG Thr	1016	
GGA Gly	CTG Leu	TCT Ser	CGC Arg 245	GTA Val	TCA Ser	GAC Asp	CAC His	AAG Lys 250	CAC His	CAT His	CCC Pro	AGT Ser	GAT Asp 255	GTT Val	CTG Leu	1064	
GCA Ala	GGA Gly	TTT Phe 260	GCT Ala	CAA Gln	GGA Gly	GCC Ala	CTG Leu 265	GTG Val	GCC Ala	TGC Cys	TGC Cys	ATA Ile 270	GTT Val	TTC Phe	TTC Phe	1112	
GTG Val	TCT Ser 275	GAC Asp	CTC Leu	TTC Phe	AAG Lys	ACT Thr 280	AAG Lys	ACG Thr	ACG Thr	CTC Leu	TCC Ser 285	CTG Leu	CCT Pro	GCC Ala	CCT Pro	1160	
GCT Ala 290	ATC Ile	CGG Arg	AAG Lys	GAA Glu	ATC Ile 295	CTT Leu	TCA Ser	CCT Pro	GTG Val	GAC Asp 300	ATT Ile	ATT Ile	GAC Asp	AGG Arg	AAC Asn 305	1208	
AAT Asn	CAC His	CAC His	AAC Asn 310	ATG Met	ATG Met	TAGGTGCCAC			CCACCTCCTG			AGCTGTTTTT				1256	
GTAAAATGAC			TGCTGACAGC			AAGTTCTTGC			TGCTCTCCAA			TCTCATCAGA			CAGTAGAATG		1316
TAGGGAAAAA			CTTTTGCCCG			ACTGATTTTT			AAAAAAAAAA			AAAAAA					1362

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Gln	Asn	Tyr	Lys	Tyr	Asp	Lys	Ala	Ile	Val	Pro	Glu	Ser	Lys	Asn	1	5	10	15
Gly	Gly	Ser	Pro	Ala	Leu	Asn	Asn	Asn	Pro	Arg	Arg	Ser	Gly	Ser	Lys	20	25	30	
Arg	Val	Leu	Leu	Ile	Cys	Leu	Asp	Leu	Phe	Cys	Leu	Phe	Met	Ala	Gly	35	40	45	
Leu	Pro	Phe	Leu	Ile	Ile	Glu	Thr	Ser	Thr	Ile	Lys	Pro	Tyr	His	Arg	50	55	60	
Gly	Phe	Tyr	Cys	Asn	Asp	Glu	Ser	Ile	Lys	Tyr	Pro	Leu	Lys	Thr	Gly	65	70	75	80
Glu	Thr	Ile	Asn	Asp	Ala	Val	Leu	Cys	Ala	Val	Gly	Ile	Val	Ile	Ala	85	90	95	
Ile	Leu	Ala	Ile	Ile	Thr	Gly	Glu	Phe	Tyr	Arg	Ile	Tyr	Tyr	Leu	Lys	100	105	110	
Lys	Ser	Arg	Ser	Thr	Ile	Gln	Asn	Pro	Tyr	Val	Ala	Ala	Leu	Tyr	Lys	115	120	125	
Gln	Val	Gly	Cys	Phe	Leu	Phe	Gly	Cys	Ala	Ile	Ser	Gln	Ser	Phe	Thr	130	135	140	
Asp	Ile	Ala	Lys	Val	Ser	Ile	Gly	Arg	Leu	Arg	Pro	His	Phe	Leu	Ser	145	150	155	160
Val	Cys	Asn	Pro	Asp	Phe	Ser	Gln	Ile	Asn	Cys	Ser	Glu	Gly	Tyr	Ile	165	170	175	
Gln	Asn	Tyr	Arg	Cys	Arg	Gly	Asp	Asp	Ser	Lys	Val	Gln	Glu	Ala	Arg	180	185	190	
Lys	Ser	Phe	Phe	Ser	Gly	His	Ala	Ser	Phe	Ser	Met	Tyr	Thr	Met	Leu	195	200	205	
Tyr	Leu	Val	Leu	Tyr	Leu	Gln	Ala	Arg	Phe	Thr	Trp	Arg	Gly	Ala	Arg	210	215	220	
Leu	Leu	Arg	Pro	Leu	Leu	Gln	Phe	Thr	Leu	Ile	Met	Met	Ala	Phe	Tyr	225	230	235	240
Thr	Gly	Leu	Ser	Arg	Val	Ser	Asp	His	Lys	His	His	Pro	Ser	Asp	Val	245	250	255	
Leu	Ala	Gly	Phe	Ala	Gln	Gly	Ala	Leu	Val	Ala	Cys	Cys	Ile	Val	Phe	260	265	270	
Phe	Val	Ser	Asp	Leu	Phe	Lys	Thr	Lys	Thr	Thr	Leu	Ser	Leu	Pro	Ala	275	280	285	
Pro	Ala	Ile	Arg	Lys	Glu	Ile	Leu	Ser	Pro	Val	Asp	Ile	Ile	Asp	Arg	290	295	300	

Asn Asn His His Asn Met Met
305 310

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 4..833

- (ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 4..833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACC	ATG	CAG	CGG	AGG	TGG	GTC	TTC	GTG	CTG	CTC	GAC	GTG	CTG	TGC	TTA	48
Met	Gln	Arg	Arg	Trp	Val	Phe	Val	Leu	Leu	Asp	Val	Leu	Cys	Leu		
1				5					10					15		
CTG	GTC	GCC	TCC	CTG	CCC	TTC	GCT	ATC	CTG	ACG	CTG	GTG	AAC	GCC	CCG	96
Leu	Val	Ala	Ser	Leu	Pro	Phe	Ala	Ile	Leu	Thr	Leu	Val	Asn	Ala	Pro	
			20					25						30		
TAC	AAG	CGA	GGA	TTT	TAC	TGC	GGG	GAT	GAC	TCC	ATC	CGG	TAC	CCC	TAC	144
Tyr	Lys	Arg	Gly	Phe	Tyr	Cys	Gly	Asp	Asp	Ser	Ile	Arg	Tyr	Pro	Tyr	
			35				40						45			
CGT	CCA	GAT	ACC	ATC	ACC	CAC	GGG	CTC	ATG	GCT	GGG	GTC	ACC	ATC	ACG	192
Arg	Pro	Asp	Thr	Ile	Thr	His	Gly	Leu	Met	Ala	Gly	Val	Thr	Ile	Thr	
		50				55						60				
GCC	ACC	GTC	ATC	CTT	GTC	TCG	GCC	GGG	GAA	GCC	TAC	CTG	GTG	TAC	ACA	240
Ala	Thr	Val	Ile	Leu	Val	Ser	Ala	Gly	Glu	Ala	Tyr	Leu	Val	Tyr	Thr	
	65				70						75					
GAC	CGG	CTC	TAT	TCT	CGC	TCG	GAC	TTC	AAC	AAC	TAC	GTG	GCT	GCT	GTA	288
Asp	Arg	Leu	Tyr	Ser	Arg	Ser	Asp	Phe	Asn	Asn	Tyr	Val	Ala	Ala	Val	
80				85					90					95		
TAC	AAG	GTG	CTG	GGG	ACC	TTC	CTG	TTT	GGG	GCT	GCC	GTG	AGC	CAG	TCT	336
Tyr	Lys	Val	Leu	Gly	Thr	Phe	Leu	Phe	Gly	Ala	Ala	Val	Ser	Gln	Ser	
			100					105						110		
CTG	ACA	GAC	CTG	GCC	AAG	TAC	ATG	ATT	GGG	CGT	CTG	AAG	CCC	AAC	TTC	384
Leu	Thr	Asp	Leu	Ala	Lys	Tyr	Met	Ile	Gly	Arg	Leu	Lys	Pro	Asn	Phe	
			115				120						125			
CTA	GCC	GTC	TGC	GAC	CCC	GAC	TGG	AGC	CGG	GTC	AAC	TGC	TCG	GTC	TAT	432
Leu	Ala	Val	Cys	Asp	Pro	Asp	Trp	Ser	Arg	Val	Asn	Cys	Ser	Val	Tyr	
	130					135				140						
GTG	CAG	CTG	GAG	AAG	GTG	TGC	AGG	GGA	AAC	CCT	GCT	GAT	GTC	ACC	GAG	480
Val	Gln	Leu	Glu	Lys	Val	Cys	Arg	Gly	Asn	Pro	Ala	Asp	Val	Thr	Glu	
	145				150					155						
GCC	AGG	TTG	TCT	TTC	TAC	TCG	GGA	CAC	TCT	TCC	TTT	GGG	ATG	TAC	TGC	528
Ala	Arg	Leu	Ser	Phe	Tyr	Ser	Gly	His	Ser	Ser	Phe	Gly	Met	Tyr	Cys	
160					165				170						175	

ATG GTG TTC TTG GCG CTG TAT GTG CAG GCA CGA CTC TGT TGG AAG TGG	576
Met Val Phe Leu Ala Leu Tyr Val Gln Ala Arg Leu Cys Trp Lys Trp	
180 185 190	
GCA CGG CTG CTG CGA CCC ACA GTC CAG TTC TTC CTG GTG GCC TTT GCC	624
Ala Arg Leu Leu Arg Pro Thr Val Gln Phe Phe Leu Val Ala Phe Ala	
195 200 205	
CTC TAC GTG GGC TAC ACC CGC GTG TCT GAT TAC AAA CAC CAC TGG AGC	672
Leu Tyr Val Gly Tyr Thr Arg Val Ser Asp Tyr Lys His His Trp Ser	
210 215 220	
GAT GTC CTT GTT GGC CTC CTG CAG GGG GCA CTG GTG GCT GCC CTC ACT	720
Asp Val Leu Val Gly Leu Leu Gln Gly Ala Leu Val Ala Ala Leu Thr	
225 230 235	
GTC TGC TAC ATC TCA GAC TTC TTC AAA GCC CGA CCC CCA CAG CAC TGT	768
Val Cys Tyr Ile Ser Asp Phe Phe Lys Ala Arg Pro Pro Gln His Cys	
240 245 250 255	
CTG AAG GAG GAG GAG CTG GAA CGG AAG CCC AGC CTG TCA CTG ACG TTG	816
Leu Lys Glu Glu Glu Leu Glu Arg Lys Pro Ser Leu Ser Leu Thr Leu	
260 265 270	
ACC CTG GGG CGA GGC TG ACCACAACCA CTTATGGGAT ACCCGCACTC	863
Thr Leu Gly Arg Gly	
275	
TTCTTCCTGA GGCCGGACCC CGCCCAGGCA GGGAGCTGCT GTGAGTCCAG CTGATGCCCCA	923
CCCAGGTGGT CCCTCCAGCC TGGTTAGGCA CTGAGGGTTC TGGACGGGCT CCAGGAACCC	983
TGGGCTGATG GGAGCAGTGA GCGGTTCCGC TGCCCCCTGC CCTGCACTGG ACCAGGAGTC	1043
TGGAGATGCC TGGGTAGCCC TCAGCATTTG GAGGGGAACC TGTTCCTGTC GGTCCCCAAA	1103
TATCCCCTTC TTTTATGGG GTTAAGGAAG GGACCGAGAG ATCAGATAGT TGCTGTTTTG	1163
TAAATGTAA TGTATATGTG GTTTTATAGTA AAATAGGGCA CCTGTTTCAC AAAAAAAAAA	1223
AAAAAAAAA	1232

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 276 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gln Arg Arg Trp Val Phe Val Leu Leu Asp Val Leu Cys Leu Leu	
1 5 10 15	
Val Ala Ser Leu Pro Phe Ala Ile Leu Thr Leu Val Asn Ala Pro Tyr	
20 25 30	
Lys Arg Gly Phe Tyr Cys Gly Asp Asp Ser Ile Arg Tyr Pro Tyr Arg	
35 40 45	
Pro Asp Thr Ile Thr His Gly Leu Met Ala Gly Val Thr Ile Thr Ala	
50 55 60	

Thr Val Ile Leu Val Ser Ala Gly Glu Ala Tyr Leu Val Tyr Thr Asp
65 70 75 80

Arg Leu Tyr Ser Arg Ser Asp Phe Asn Asn Tyr Val Ala Ala Val Tyr
85 90 95

Lys Val Leu Gly Thr Phe Leu Phe Gly Ala Ala Val Ser Gln Ser Leu
100 105 110

Thr Asp Leu Ala Lys Tyr Met Ile Gly Arg Leu Lys Pro Asn Phe Leu
115 120 125

Ala Val Cys Asp Pro Asp Trp Ser Arg Val Asn Cys Ser Val Tyr Val
130 135 140

Gln Leu Glu Lys Val Cys Arg Gly Asn Pro Ala Asp Val Thr Glu Ala
145 150 155 160

Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Gly Met Tyr Cys Met
165 170 175

Val Phe Leu Ala Leu Tyr Val Gln Ala Arg Leu Cys Trp Lys Trp Ala
180 185 190

Arg Leu Leu Arg Pro Thr Val Gln Phe Phe Leu Val Ala Phe Ala Leu
195 200 205

Tyr Val Gly Tyr Thr Arg Val Ser Asp Tyr Lys His His Trp Ser Asp
210 215 220

Val Leu Val Gly Leu Leu Gln Gly Ala Leu Val Ala Ala Leu Thr Val
225 230 235 240

Cys Tyr Ile Ser Asp Phe Phe Lys Ala Arg Pro Pro Gln His Cys Leu
245 250 255

Lys Glu Glu Glu Leu Glu Arg Lys Pro Ser Leu Ser Leu Thr Leu Thr
260 265 270

Leu Gly Arg Gly
275

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Phe Asp Lys Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Ile Cys
1 5 10 15

Val Leu Leu Ala Gly Leu Pro Phe Ala Ile Leu Thr Ser Arg His Thr
20 25 30

Pro Phe Gln Arg Gly Ile Phe Cys Asn Asp Asp Ser Ile Lys Tyr Pro
35 40 45

Tyr Lys Glu Asp Thr Ile Pro Tyr Ala Leu Leu Gly Gly Ile Val Ile
50 55 60

Pro Phe Cys Ile Ile Val Met Ser Ile Gly Glu Ser Leu Ser Val Tyr
65 70 75 80

Phe Asn Val Leu His Ser Asn Ser Phe Val Gly Asn Pro Tyr Ile Ala
85 90 95

Thr Ile Tyr Lys Ala Val Gly Ala Phe Leu Phe Gly Val Ser Ala Ser
100 105 110

Gln Ser Leu Thr Asp Ile Ala Lys Tyr Thr Ile Gly Ser Leu Arg Pro
115 120 125

His Phe Leu Ala Ile Cys Asn Pro Asp Trp Ser Lys Ile Asn Cys Ser
130 135 140

Asp Gly Tyr Ile Glu Asp Tyr Ile Cys Gln Gly Asn Glu Glu Lys Val
145 150 155 160

Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met
165 170 175

Tyr Cys Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly
180 185 190

Asp Trp Ala Arg Leu Leu Arg Pro Met Leu Gln Phe Gly Leu Ile Ala
195 200 205

Phe Ser Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His
210 215 220

Trp Ser Asp Val Thr Val Gly Leu Ile Gln Gly Ala Ala Met Ala Ile
225 230 235 240

Leu Val Ala Leu Tyr Val Ser Asp Phe Phe Lys Asp Thr His Ser Tyr
245 250 255

Lys Glu Arg Lys Glu Glu Asp Pro His Thr Thr Leu His Glu Thr Ala
260 265 270

Ser Ser Arg Asn Tyr Ser Thr Asn His Glu Pro
275 280

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 284 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Phe Asp Lys Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys
1 5 10 15

Val Leu Leu Ala Gly Leu Pro Phe Ala Ile Leu Thr Ser Arg His Thr
20 25 30

Pro Phe Gln Arg Gly Val Phe Cys Asn Asp Glu Ser Ile Lys Tyr Pro
35 40 45

Tyr Lys Glu Asp Thr Ile Pro Tyr Ala Leu Leu Gly Gly Ile Ile Ile
50 55 60

Pro	Phe	Ser	Ile	Ile	Val	Ile	Ile	Leu	Gly	Glu	Thr	Leu	Ser	Val	Tyr	65	70	75	80
Cys	Asn	Leu	Leu	His	Ser	Asn	Ser	Phe	Ile	Arg	Asn	Asn	Tyr	Ile	Ala	85	90	95	
Thr	Ile	Tyr	Lys	Ala	Ile	Gly	Thr	Phe	Leu	Phe	Gly	Ala	Ala	Ala	Ser	100	105	110	
Gln	Ser	Leu	Thr	Asp	Ile	Ala	Lys	Tyr	Ser	Ile	Gly	Arg	Leu	Arg	Pro	115	120	125	
His	Phe	Leu	Asp	Val	Cys	Asp	Pro	Asp	Trp	Ser	Lys	Ile	Asn	Cys	Ser	130	135	140	
Asp	Gly	Tyr	Ile	Glu	Tyr	Tyr	Ile	Cys	Arg	Gly	Asn	Ala	Glu	Arg	Val	145	150	155	160
Lys	Glu	Gly	Arg	Leu	Ser	Phe	Tyr	Ser	Gly	His	Ser	Ser	Phe	Ser	Met	165	170	175	
Tyr	Cys	Met	Leu	Phe	Val	Ala	Leu	Tyr	Leu	Gln	Ala	Arg	Met	Lys	Gly	180	185	190	
Asp	Trp	Ala	Arg	Leu	Leu	Arg	Pro	Thr	Leu	Gln	Phe	Gly	Leu	Val	Ala	195	200	205	
Val	Ser	Ile	Tyr	Val	Gly	Leu	Ser	Arg	Val	Ser	Asp	Tyr	Lys	His	His	210	215	220	
Trp	Ser	Asp	Val	Leu	Thr	Gly	Leu	Ile	Gln	Gly	Ala	Leu	Val	Ala	Ile	225	230	235	240
Leu	Val	Ala	Val	Tyr	Val	Ser	Asp	Phe	Phe	Lys	Glu	Arg	Thr	Ser	Phe	245	250	255	
Lys	Glu	Arg	Lys	Glu	Glu	Asp	Ser	His	Thr	Thr	Leu	His	Glu	Thr	Pro	260	265	270	
Thr	Thr	Gly	Asn	His	Tyr	Pro	Ser	Asn	His	Gln	Pro					275	280		

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 285 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Phe	Asp	Lys	Thr	Arg	Leu	Pro	Tyr	Val	Ala	Leu	Asp	Val	Leu	Cys	1	5	10	15
Val	Leu	Leu	Ala	Ser	Met	Pro	Met	Ala	Val	Leu	Lys	Leu	Gly	Gln	Ile	20	25	30	
Tyr	Pro	Phe	Gln	Arg	Gly	Phe	Phe	Cys	Lys	Asp	Asn	Ser	Ile	Asn	Tyr	35	40	45	
Pro	Tyr	His	Asp	Ser	Thr	Ala	Ala	Ser	Thr	Val	Leu	Ile	Leu	Val	Gly	50	55	60	

Val	Gly	Leu	Pro	Val	Ser	Ser	Ile	Ile	Leu	Gly	Glu	Thr	Leu	Ser	Val
65					70					75					80
Tyr	Cys	Asn	Leu	Leu	His	Ser	Asn	Ser	Phe	Ile	Arg	Asn	Asn	Tyr	Ile
				85					90					95	
Ala	Thr	Ile	Tyr	Lys	Ala	Ile	Gly	Thr	Phe	Leu	Phe	Gly	Ala	Ala	Ala
			100					105					110		
Ser	Gln	Ser	Leu	Thr	Asp	Ile	Ala	Lys	Tyr	Ser	Ile	Gly	Arg	Leu	Arg
			115				120					125			
Pro	His	Phe	Leu	Asp	Val	Cys	Asp	Pro	Asp	Trp	Ser	Lys	Ile	Asn	Cys
	130					135					140				
Ser	Asp	Gly	Tyr	Ile	Glu	Tyr	Tyr	Ile	Cys	Arg	Gly	Asn	Ala	Glu	Arg
145					150					155					160
Val	Lys	Glu	Gly	Arg	Leu	Ser	Phe	Tyr	Ser	Gly	His	Ser	Ser	Phe	Ser
				165					170						175
Met	Tyr	Cys	Met	Leu	Phe	Val	Ala	Leu	Tyr	Leu	Gln	Ala	Arg	Met	Lys
			180					185					190		
Gly	Asp	Trp	Ala	Arg	Leu	Leu	Arg	Pro	Thr	Leu	Gln	Phe	Gly	Leu	Val
		195					200						205		
Ala	Val	Ser	Ile	Tyr	Val	Gly	Leu	Ser	Arg	Val	Ser	Asp	Tyr	Lys	His
			210			215					220				
His	Trp	Ser	Asp	Val	Leu	Thr	Gly	Leu	Ile	Gln	Gly	Ala	Leu	Val	Ala
225					230					235					240
Ile	Leu	Val	Ala	Val	Tyr	Val	Ser	Asp	Phe	Phe	Lys	Glu	Arg	Thr	Ser
				245					250					255	
Phe	Lys	Glu	Arg	Lys	Glu	Glu	Asp	Ser	His	Thr	Thr	Leu	His	Glu	Thr
			260					265					270		
Pro	Thr	Thr	Gly	Asn	His	Tyr	Pro	Ser	Asn	His	Gln	Pro			
			275				280					285			

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 311 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Gln	Asn	Tyr	Lys	Tyr	Asp	Lys	Ala	Ile	Val	Pro	Glu	Ser	Lys	Asn
1				5					10					15	
Gly	Gly	Ser	Pro	Ala	Leu	Asn	Asn	Asn	Pro	Arg	Arg	Ser	Gly	Ser	Lys
			20					25					30		
Arg	Val	Leu	Leu	Ile	Cys	Leu	Asp	Leu	Phe	Cys	Leu	Phe	Met	Ala	Gly
			35				40					45			
Leu	Pro	Phe	Leu	Ile	Ile	Glu	Thr	Ser	Thr	Ile	Lys	Pro	Tyr	His	Arg
			50			55					60				

Gly Phe Tyr Cys Asn Asp Glu Ser Ile Lys Tyr Pro Leu Lys Thr Gly
65 70 75 80

Glu Thr Ile Asn Asp Ala Val Leu Cys Ala Val Gly Ile Val Ile Ala
85 90 95

Ile Leu Ala Ile Ile Thr Gly Glu Phe Tyr Arg Ile Tyr Tyr Leu Lys
100 105 110

Lys Ser Arg Ser Thr Ile Gln Asn Pro Tyr Val Ala Ala Leu Tyr Lys
115 120 125

Gln Val Gly Cys Phe Leu Phe Gly Cys Ala Ile Ser Gln Ser Phe Thr
130 135 140

Asp Ile Ala Lys Val Ser Ile Gly Arg Leu Arg Pro His Phe Leu Ser
145 150 155 160

Val Cys Asn Pro Asp Phe Ser Gln Ile Asn Cys Ser Glu Gly Tyr Ile
165 170 175

Gln Asn Tyr Arg Cys Arg Gly Asp Asp Ser Lys Val Gln Glu Ala Arg
180 185 190

Lys Ser Phe Phe Ser Gly His Ala Ser Phe Ser Met Tyr Thr Met Leu
195 200 205

Tyr Leu Val Leu Tyr Leu Gln Ala Arg Phe Thr Trp Arg Gly Ala Arg
210 215 220

Leu Leu Arg Pro Leu Leu Gln Phe Thr Leu Ile Met Met Ala Phe Tyr
225 230 235 240

Thr Gly Leu Ser Arg Val Ser Asp His Lys His His Pro Ser Asp Val
245 250 255

Leu Ala Gly Phe Ala Gln Gly Ala Leu Val Ala Cys Cys Ile Val Phe
260 265 270

Phe Val Ser Asp Leu Phe Lys Thr Lys Thr Thr Leu Ser Leu Pro Ala
275 280 285

Pro Ala Ile Arg Lys Glu Ile Leu Ser Pro Val Asp Ile Ile Asp Arg
290 295 300

Asn Asn His His Asn Met Met
305 310

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 276 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Gln Arg Arg Trp Val Phe Val Leu Leu Asp Val Leu Cys Leu Leu
1 5 10 15

Val Ala Ser Leu Pro Phe Ala Ile Leu Thr Leu Val Asn Ala Pro Tyr
20 25 30

Lys Arg Gly Phe Tyr Cys Gly Asp Asp Ser Ile Arg Tyr Pro Tyr Arg
35 40 45

Pro Asp Thr Ile Thr His Gly Leu Met Ala Gly Val Thr Ile Thr Ala
50 55 60

Thr Val Ile Leu Val Ser Ala Gly Glu Ala Tyr Leu Val Tyr Thr Asp
65 70 75 80

Arg Leu Tyr Ser Arg Ser Asp Phe Asn Asn Tyr Val Ala Ala Val Tyr
85 90 95

Lys Val Leu Gly Thr Phe Leu Phe Gly Ala Ala Val Ser Gln Ser Leu
100 105 110

Thr Asp Leu Ala Lys Tyr Met Ile Gly Arg Leu Lys Pro Asn Phe Leu
115 120 125

Ala Val Cys Asp Pro Asp Trp Ser Arg Val Asn Cys Ser Val Tyr Val
130 135 140

Gln Leu Glu Lys Val Cys Arg Gly Asn Pro Ala Asp Val Thr Glu Ala
145 150 155 160

Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Gly Met Tyr Cys Met
165 170 175

Val Phe Leu Ala Leu Tyr Val Gln Ala Arg Leu Cys Trp Lys Trp Ala
180 185 190

Arg Leu Leu Arg Pro Thr Val Gln Phe Phe Leu Val Ala Phe Ala Leu
195 200 205

Tyr Val Gly Tyr Thr Arg Val Ser Asp Tyr Lys His His Trp Ser Asp
210 215 220

Val Leu Val Gly Leu Leu Gln Gly Ala Leu Val Ala Ala Leu Thr Val
225 230 235 240

Cys Tyr Ile Ser Asp Phe Phe Lys Ala Arg Pro Pro Gln His Cys Leu
245 250 255

Lys Glu Glu Glu Leu Glu Arg Lys Pro Ser Leu Ser Leu Thr Leu Thr
260 265 270

Leu Gly Arg Gly
275

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGCTCTAGAT ATTAATAGTA ATCAATTAC

29

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCTCACGCAT GCACCATGGT AATAGC

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(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTGCATGCG TGAGGCTCCG GTGC

24

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTAGTTTTCA CGGTACCTGA AATGGAAG

28

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGCATGGTAC CATGTTTGAC AAGACGCGGC

30

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CATATGTAGT ATTCAATGTA ACC

23

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGATGGCTAG CATGCAGAGA AGATGGGTCT TCGTGCTGCT CGACGTG

47

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AGTGCGGGAT CCCATAAGTG GTTG

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Atty. Docket No: 077319/0125

In re patent application of

David W. LEUNG et al.

Serial No. 08/842,827

Group Art Unit: 1801

Filed: April 17, 1997

Examiner: Unassigned

For: HUMAN PHOSPHATIDIC ACID PHOSPHATASE

PRELIMINARY AMENDMENT

Assistant Commissioner for Patents
Washington, D.C. 20231
Box SEQUENCE

Sir:

In response to the Notice to Comply With Requirements for Applications Containing Sequence Disclosures mailed June 9, 1997, please amend the application as follows:

IN THE SPECIFICATION:

Page 3, line 22, after "284" insert --(SEQ ID NO:2)--;
line 24, after "285" insert --(SEQ ID NO:4)--;
line 25, after "276" insert --(SEQ ID NO:8)--;
line 30, after "284" insert --(SEQ ID NO:2)--;
line 31, after "285" insert --(SEQ ID NO:4)--;
line 33, after "276" insert --(SEQ ID NO:8)--.

Page 4, line 23, after "sequence" insert --(SEQ ID NOS:1 and 2)--;
line 26, after "sequence" insert --(SEQ ID NOS:3 and 4)--;
line 29, after "sequence" insert --(SEQ ID NOS:5 and 6)--;
line 32, after "sequence" insert --(SEQ ID NOS:7 and 8)--;

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line 33, after "sequences" insert --(SEQ ID NOS:9-13)--.

Page 7, line 35, after "4" insert --(SEQ ID NOS:2, 4, 6 and 8)--.

Page 10, line 18, after "1193" insert --of SEQ ID NO:1--;

line 19, after "1196" insert --of SEQ ID NO:3--; delete "amino acid number";

line 20, delete "1 to amino acid number 311" and insert --nucleotide number 294 to nucleotide number 1226 of SEQ ID NO:5--;

line 21, after "833" insert --of SEQ ID NO:7--.

Page 11, line 12, after "4" insert --(SEQ ID NOS:1, 3, 5 and 7)--.

Page 14, line 31, after "3'" insert --(SEQ ID NO:14)--;
line 32, after "3'" insert --(SEQ ID NO:15)--;
line 36, after "3'" insert --(SEQ ID NO:16)--.

Page 15, line 1, after "3'" insert --(SEQ ID NO:17)--.

Page 18, line 34, after "3'" insert --(SEQ ID NO:18)--;
line 35, after "3'" insert --(SEQ ID NO:19)--.

Page 19, line 25, after "3'" insert --(SEQ ID NO:14)--;
line 26, after "3'" insert --(SEQ ID NO:15)--;
line 30, after "3'" insert --(SEQ ID NO:16)--;
line 31, after "3'" insert --(SEQ ID NO:17)--.

Page 20, line 4, after "3'" insert --(SEQ ID NO:20)--;
line 6, after "3'" insert --(SEQ ID NO:21)--;

Serial No. 08/842,827

line 15, before "respectively" insert --(SEQ ID NOS:1, 3, 5 and 7)--;

line 21, after "4" insert --, SEQ ID NOS:2, 4, 6 and 8--.

Page 22, at the end of the specification, before the claims, insert the printed Sequence Listing submitted concurrently herewith, and renumber pages 1-19 of the Sequence Listing as pages 23-41 of the specification.

IN THE CLAIMS:

Please renumber pages 23-24 as pages 42-43 and amend the claims as follows.

1. (Amended) An isolated polynucleotide encoding human phosphatidic acid phosphatase wherein said polynucleotide encodes a protein comprising a polypeptide sequence selected from the group consisting of (i) the sequence at amino acid number 1 to amino acid number 284 in Figure 1 (SEQ ID NO:2), (ii) the sequence at amino acid number 1 to amino acid number 285 in Figure 2 (SEQ ID NO:4), and (iii) the sequence at amino acid number 1 to amino acid number 276 in Figure 4 (SEQ ID NO:8).

2. (Amended) An isolated human phosphatidic acid phosphatase protein, wherein said protein comprises a polypeptide sequence selected from the group consisting of (i) the sequence at amino acid number 1 to amino acid number 284 in Figure 1 (SEQ ID NO:2), (ii) the sequence at amino acid number 1 to amino acid number 285 in Figure 2 (SEQ ID NO:4), and (iii) the sequence at amino acid number 1 to amino acid number 276 in Figure 4 (SEQ ID NO:8).

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4. (Amended) The method of claim 3, wherein said polynucleotide encoding human phosphatidic acid is selected from the group consisting of (i) the sequence at amino acid number 1 to amino acid number 284 in Figure 1 (SEQ ID NO:2), (ii) the sequence at amino acid number 1 to amino acid number 285 in Figure 2 (SEQ ID NO:4), (iii) the sequence at amino acid number 1 to amino acid number 311 in Figure 3 (SEQ ID NO:6), and (iv) the sequence at amino acid number 1 to amino acid number 276 in Figure 4 (SEQ ID NO:8).

Claim 6, line 3, after "1" insert --(SEQ ID NO:2)--.

Claim 7, line 3, after "2" insert --(SEQ ID NO:4)--.

Claim 8, line 3, after "3" insert --(SEQ ID NO:6)--.

Claim 9, line 3, after "4" insert --(SEQ ID NO:8)--.

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REMARKS

Applicants submit this Preliminary Amendment to insert required references to SEQ ID NOS of the Sequence Listing filed concurrently herewith, to indicate the insertion point for the Sequence Listing, and to effect the necessary changes in pagination. Applicants also have corrected a typographical error appearing at page 10, lines 19-20. Applicants respectfully request examination on the merits of this application.

It is believed that no additional fees are required; however, the Commissioner is hereby authorized to charge any deficiency or credit any overpayment to Deposit Account No. 19-0741. It is further believed that no additional petition for an extension of time under 37 C.F.R. § 1.136 is required. However, should such a petition be required, applicant hereby petitions the Commissioner for an extension of time, and authorizes the Commissioner to charge the necessary petition fee to Deposit Account No. 19-0741.

Respectfully submitted,

5 August 1997
Date

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DECLARATION AND POWER OF ATTORNEY

As a below named inventor, I hereby declare that:

My residence, post office address, and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

HUMAN PHOSPHATIDIC ACID PHOSPHATASE

the specification of which is attached hereto unless the following box is checked:

☒ was filed on April 17, 1997 as United States Application Number or PCT International Application Number 08/842,827 and was amended on _____ (if applicable).

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is known by me to be material to patentability as defined in Title 37, Code of Federal Regulations § 1.56.

I hereby claim foreign priority benefits under Title 35, United States Code, § 119(a)-(d) or § 365(b) of any foreign application(s) for patent or inventor's certificate, or § 365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below any foreign application for patent or inventor's certificate, or PCT International application having a filing date before that of the application on which priority is claimed:

PRIOR FOREIGN APPLICATION(S)

NUMBER	COUNTRY	DAY/MONTH/YEAR FILED	PRIORITY CLAIMED

I hereby claim the benefit under Title 35, United States Code § 119(e) of any United States provisional application(s) listed below.

APPLICATION NO.	FILING DATE


I hereby claim the benefit under Title 35, United States Code, § 120 of any United States application(s), or § 365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of Title 35, United States Code, § 112, I acknowledge the duty to disclose information which is known by me to be material to patentability as defined in Title 37, Code of Federal Regulations § 1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application:

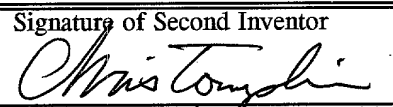
APPLICATION SERIAL NO.	FILING DATE	STATUS: PATENTED, PENDING, ABANDONED

I hereby appoint as my attorneys, with full powers of substitution and revocation, to prosecute this application and transact all business in the Patent and Trademark Office connected therewith: Stephen A. Bent, Reg. No. 29,768; David A. Blumenthal, Reg. No. 26,257; William T. Ellis, Reg. No. 26,874; John J. Feldhaus, Reg. No. 28,822; Patricia D. Granados, Reg. No. 33,683; John P. Isacson, Reg. No. 33,715; Donald D. Jeffery, Reg. No. 19,980; Eugene M. Lee, Reg. No. 32,039; Peter G. Mack, Reg. No. 26,001; Brian J. McNamara, Reg. No. 32,789; Sybil Meloy, Reg. No. 22,749; George E. Quillin, Reg. No. 32,792; Colin G. Sandercock, Reg. No. 31,298; Bernhard D. Saxe, Reg. No. 28,665; Charles F. Schill, Reg. No. 27,590; Richard L. Schwaab, Reg. No. 25,479; Arthur Schwartz, Reg. No. 22,115; Harold C. Wegner, Reg. No. 25,258.

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Address telephone communications to John P. Isacson at (202) 672-5300.

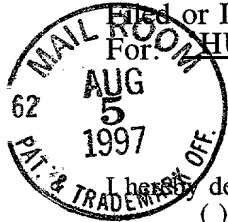
I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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077319/0125

Applicant or Patentee: David W. LEUNG et al
Serial or Patent No.: 08/842,827 Atty. Dkt. No. 077319/0125
Filed or Issued: April 17, 1997
For: HUMAN PHOSPHATIDIC ACID PHOSPHATASE



VERIFIED STATEMENT (DECLARATION) CLAIMING SMALL ENTITY STATUS
(37 CFR 1.9(f) AND 1.27 (c)) — SMALL BUSINESS CONCERN

I hereby declare that I am
☐ the owner of the small business concern identified below:
☐ an official of the small business concern empowered to act on behalf of the concern identified below:

NAME OF CONCERN CELL THERAPEUTICS, INC.
ADDRESS OF CONCERN Suite #401, 201 Elliott Avenue, West, Seattle, Washington, 98119

I hereby declare that the above-identified small business concern qualifies as a small business concern as defined in 13 CFR 121.3-18 and reproduced in 37 CFR 1.9(d), for purposes of paying reduced fees under section 41(a) and (b) of Title 35, United States Code, in that the number of employees of the concern, including those of its affiliates, does not exceed 500 persons. For purposes of this statement, (1) the number of employees of the business concern is the average over the previous fiscal year of the concern of the persons employed on a full-time, part-time or temporary basis during each of the pay periods of the fiscal year, and (2) concerns are affiliates of each other when either, directly or indirectly, one concern controls or has the power to control the other, or a third party or parties controls or has the power to control both.

I hereby declare that rights under contract or law have been conveyed to and remain with the small business concern identified above with regard to the invention, entitled HUMAN PHOSPHATIDIC ACID PHOSPHATASE by inventor(s) David W. LEUNG et al. described in

☐ the specification filed herewith
☒ application serial no. 08/842,827, filed April 17, 1997
☐ patent no. _____, issued _____

If the rights held by the above-identified small business concern are not exclusive, each individual, concern or organization having rights to the invention is listed below* and no rights to the invention are held by any person, other than the inventor, who would not qualify as an independent inventor under 37 CFR 1.9(c) if that person made the invention, or by any concern which would not qualify as a small business concern under 37 CFR 1.9(d) or a nonprofit organization under 37 CFR 1.9(e). * NOTE: Separate verified statements are required from each named person, concern or organization having rights to the invention averring to their status as small entities: (37 CFR 1.27)

NAME: _____
ADDRESS: _____
☐ INDIVIDUAL ☐ SMALL BUSINESS CONCERN ☐ NONPROFIT CORPORATION

NAME: _____
ADDRESS: _____
☐ INDIVIDUAL ☐ SMALL BUSINESS CONCERN ☐ NONPROFIT CORPORATION

I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small entity is no longer appropriate: (37 CFR 1.28(b)).

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

NAME OF PERSON SIGNING: Maurice J. Schwarz, PhD
TITLE OF PERSON OTHER THAN OWNER: EVP, Product Development
ADDRESS OF PERSON SIGNING: 201 Elliott Avenue West, Suite 400, Seattle, WA 98119
SIGNATURE: [Signature] DATE: 7/16/97